



Figure 1

BLAST search against SwissProt



Identify gene family

ClustalW comparison with SwissProt top hit



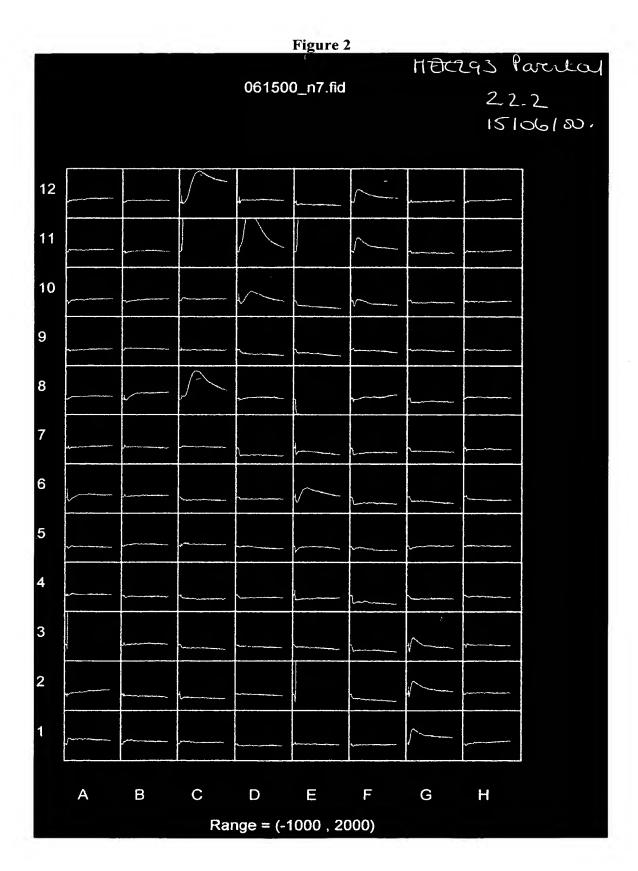
Demonstrates global alignment

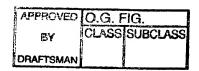
BLAST against nonredundant GPCR db



Demonstrates GPCR sub-family

-i.

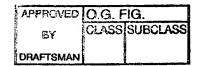




# Figure 3

## CLUSTAL W (1.74) multiple sequence alignment

NTR1_RAT PFI-002	MHLNSSVPQGTPGEPDAQPFSGPQSEMEATFLALSLSNGSGNTSESDTAGPNSDLDVNTDMEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRS * :. *::* .* *::*. * .
NTR1_RAT PFI-002	IYSKVLVTAIYLALFVVGTVGNSVTAFTLARKKSLQSLQSTVHYHLGSLALSDLLILLLA HF-FLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLG : : *:.:*::****:****.:**
NTR1_RAT PFI-002	MPVELYNFIWVHHPWAFGDAGCRGYYFLRDACTYATALNVASLSVERYLAICHPFKAKTL MPLEVY-EMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQ **:*: : : : : : : : : : : : : : : : : :
NTR1_RAT PFI-002	MSRSRTKKFISAIWLASALLAIPMLFTMGLQN-RSGDG-THPGGLVCTPIVDTATVKVVI STRRALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFII :* *: ::: : * *.*::* *:: : : * **** * :.:*
NTR1_RAT PFI-002	QVNTFMSFLFPMLVISILNTVIANKLTVMVHQAAEQGRVCTVGTHNGLEHSTFNMTIEPG QVTSFLFYLLPMTVISVLYYLMALR **.:*: :*: ** ***:* ::* :
NTR1_RAT PFI-002	RVQALRHGVLVLRAVVIAFVVCWLPYHVRRLMFCYISDEQWTTFLFDFYHYFYMLTNALF
NTR1_RAT PFI-002	YVSSAINPILYNLVSANFRQVFLSTLACLCPGWRHRRKKRPTFSRKPNSMSSNHAFSTSA
NTR1_RAT PFI-002	TRETLY



# Figure 4

CLUSTAL W (1.74) multiple sequence alignment

GPCR0244 GPCR0303	MACNGSAARGHFDPEDLNLTDEALRLKYLGPQQTELFMPICATYLLIFVVG MAGMEKLQNASWIYQQKLEDPFQKHLNSTEEYLAF-LCGPRRSHFFLPVSVVYVPIFVVG *.* : ** :.** *: **::::*:*:*: *****
GPCR0244 GPCR0303	AVGNGLTCLVILRHKAMRTPTNYYLFSLAVSDLLVLLVGLPLELYEMWHNYPFLLGVGGC VIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGC .:** *.****:*:**:**********************
GPCR0244 GPCR0303	YFRTLLFEMVCLASVLNVTALSVERYVAVVHPLQARSMVTRAHVRRVLGAVWGLAMLCSL YFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSL **: *** **: *: **: ***: ***: **
GPCR0244 GPCR0303	PNTSLHGIRQLHVPCRGPVPDSAVCMLVRPRALYNMVVQTTALLFFCLPMAIMSVLYLLI PNTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLM ****:***: :.* . **.**.* :::* :**::**: ***:::*** *:
GPCR0244 GPCR0303	GLRLRRERLLLMQEAKGRGSAAARSRYTCRLQQHDRGRRQVTKMLFVLVVVFGICWAPFH ALRLKKDKSLEADEGNANIQ-R-PCRKSVNKMLFVLVLVFAICWAPFH .***::: * :* * :* * .* * .* *:.*********
GPCR0244 GPCR0303	ADRVMWSVVSQWTDGLHLAFQHVHVISGIFFYLGSAANPVLYSLMSSRFRETFQEALC-LIDRLFFSFVEEWTESLAAVFNLVHVVSGVLFYLSSAVNPIIYNLLSRRFQAAFQNVISSF*:::*.*.:*.*.*.*: **::**:::*::*:::*::::::::
GPCR0244 GPCR0303	GACCHRLRPRHSSHSLSRMTTGSTLCDVGSLGSWVHPLAGNDGPEAQQ HKQWHSQHDPQLPPAQRNIFLTECHFVELTEDIGPQFLCQSSVHNSHLPTALSS-EQMSR  * :* * : . *: . *: * * * * * * . : . :
GPCR0244 GPCR0303	ETDPS TNYQSFHFNKT . *

GPCR0244 = NMUR1 GPCR0303 = Pfi002 AFFROVED O.G. FIG.
BY CLASS SUBCLASS
DRAFTSMAN

#### Figure 5

#### Figure 5A

Nucleotide sequence coding for PFI-002

**SEQ ID NO: 1** 

ATGGAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATC
CATTCCAGAAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGG
ACCTCGGCGCAGCCACTTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTT
TGTGGTGGGGGTCATTGGCAATGTCCTGGTGTGCCTGGTGATTCTGCAGCACC
AGGCTATGAAGACGCCCACCAACTACTACCTCTTCAGCCTGGCGGTCTCTGA
CCTCCTGGTCCTCCTTGGAATGCCCCTGGAGGTCTATGAGATGTGGCGCA
ACTACCCTTTCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGACGGCCCTCTTT
GAGACCGTGTGCTTCGCCTCCATCCTCAGCATCACCACCGTCAGCGTGGAGC
GCTACGTGGCCATCCTACACCCGTTCCGCGCCAAACTGCAGAGCACCCGGCG
CCGGGCCCTCAGGATCCTCGGCATCGTCTGGGGCTTCTCCCCAATGGGTCC
TGCCCAACACCAGCATCCATGGCATCAAGTTCCACTACTTCCCCAATGGGTCC
CTGGTCCCAGGTTCGGCCACCTGTACGGTCATCAAGCCCATGTGGATCTACA
ATTTCATCATCCAGGTCACCTCCTTCCTATTCTACCTCCCCATGACTGTCA
TCAGTGTCCTCTACTACCTCATGGCACTCAGAGTGAGTATCTAG

### Figure 5B

Amino acid sequence coding for PFI-002

#### **SEQ ID NO: 2**

MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVV GVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPF LFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGI VWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYL LPMTVISVLYYLMALRVSI

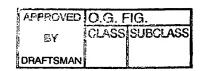


Figure 6

**SEQ ID NO: 3** ACCATGGCAGGGATGGAAAAACTT

**SEQ ID NO: 4** GCTCTGAAAGAATTCAGGTTTTG

**SEQ ID NO: 5** TCCAGAAACACCTGAACAGC

**SEQ ID NO: 6**GAGGTAGAATAGGAAGGAGG